

A. Harris

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1642

PH#77

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/274,752D

DATE: 05/01/2001

TIME: 18:10:05

Input Set : A:\A-67501.app

Output Set: N:\CRF3\05012001\I274752D.raw

ENTERED

3 <110> APPLICANT: Goetzl, Edward L.  
4 An, Songzhu  
6 <120> TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and  
7 Sphingolipids and Nucleic Acids Encoding the Same  
9 <130> FILE REFERENCE: A-67501/DJB/TAL  
11 <140> CURRENT APPLICATION NUMBER: 09/274,752D  
12 <141> CURRENT FILING DATE: 1999-03-23  
14 <160> NUMBER OF SEQ ID NOS: 29  
16 <170> SOFTWARE: PatentIn Ver. 2.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 382  
20 <212> TYPE: PRT  
21 <213> ORGANISM: Homo sapiens  
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27 Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp  
28 20 25 30  
30 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu  
31 35 40 45  
33 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His  
34 50 55 60  
36 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe  
37 65 70 75 80  
39 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr  
40 85 90 95  
42 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp  
43 100 105 110  
45 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu  
46 115 120 125  
48 Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg  
49 130 135 140  
51 Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly  
52 145 150 155 160  
54 Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp  
55 165 170 175  
57 Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val  
58 180 185 190  
60 Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr  
61 195 200 205  
63 Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu  
64 210 215 220  
66 His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val  
67 225 230 235 240  
69 Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro  
70 245 250 255  
72 Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn

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73          260          265          270
75 Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
76          275          280          285
78 Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ser Glu Met Arg Arg
79          290          295          300
81 Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
82 305          310          315          320
84 Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
85          325          330          335
87 Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
88          340          345          350
90 Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
91          355          360          365
93 Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
94          370          375          380
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98 <211> LENGTH: 1734
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
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105 atcggcttct tctataacaa cagtggcaaa gagctcagct cccactggcg gcccaaggat 180
106 gtggctcgtg tggcactggg gctgaccgtc agcgtgctgg tgctgctgac caatctgctg 240
107 gtcatagcag ccacgcctc caaccgccgc ttccaccagc ccatctacta cctgctcggc 300
108 aatctggccg cggtgacct ctccgcgggc gtggcctacc tcttctcat gttccacact 360
109 ggtccccgca cagcccgact ttcaacttgag ggctggttcc tgcggcaggg cttgctggac 420
110 acaagcctca ctgcgtcggg gccacactg ctggccatcg ccgtggagct gcaccgcagt 480
111 gtgatgtccg tgcagctgca cagccgcctg ccccggtggc gcgtggtcat gctcattgtg 540
112 ggcgtgtggg tggctgccct gggcctgggg ctgctgcctg cccactcctg gcactgcctc 600
113 tgtgccctgg accgctgctc acgcatggca ccctgctca gccgctccta tttggccgtc 660
114 tgggctctgt cgagcctgtc tgttctcctg ctcatgggtg ctgtgtacac ccgcattttc 720
115 ttctacgtgc ggcggcgagt gcagcgcagt gcagagcatg tcagctgcca cccccgtac 780
116 cgagagacca cgctcagcct ggtcaagact gttgtcatca tctggggggc gttcgtggtc 840
117 tgctggacac caggccaggt ggtactgtc ctggatggtt taggtgtga gtctgcaat 900
118 gtcttggtg tagaaaagta ctctctactg ttggccgagg ccaactcact ggtcaatgct 960
119 gctgtgtact cttgccgaga tgctgagatg cgcgcacact tccgcgcct tctctgctgc 1020
120 gcgtgcctcc gccagtcacc ccgcgagctt gtccactata cactctctgc ccagggaggt 1080
121 gccagcactc gcatcatgct tcccagaaac ggccacccac tgatgactcc acccttttag 1140
122 taccttgaac ttccagcgga cgcggcaagc aacaaatcca cagcccctga tgacttgtgg 1200
123 gtgctcctgg ctcaacccaa ccaacaggac tgactgactg gcaggacaag gtctggcatg 1260
124 gcacagcacc actgccaggc ctccccaggc acaccactct gccagggaa tgggggcttt 1320
125 gggtcactct ccactgcctg ggggagtcag atggggtgca ggaatctggc tcttcagcca 1380
126 tctcaggttt agggggtttg taacagacat tattctgttt tcaactgcgt tcttggttaa 1440
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128 gctctctcgg gccatgctac ccggtatgac tgggtaatga ggacagactg tggacacccc 1560
129 atctacctga gtctgattct ttagcagcag agactgagg gtgcagagtg tgagctggga 1620
130 aaggtttgtg gctccttgca gcctccaggg actggcctgt cccaataga attgaagcag 1680
131 tccacgggga ggggatgata caaggagtaa acctttcttt aactcaaaa aaaa 1734

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Input Set : A:\A-67501.app

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133 <210> SEQ ID NO: 3
134 <211> LENGTH: 353
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
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140 1 5 10 15
142 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
143 20 25 30
145 Arg Gln Val Ala Ser Ala Gly Ile Val Ile Leu Cys Cys Ala Ile Val
146 35 40 45
148 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
149 50 55 60
151 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
152 65 70 75 80
154 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
155 85 90 95
157 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
158 100 105 110
160 Ser Ile Thr Leu Ser Ala Ser Val Gly Ser Leu Leu Ala Ile Ala Ile
161 115 120 125
163 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Cys Lys
164 130 135 140
166 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
167 145 150 155 160
169 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
170 165 170 175
172 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
173 180 185 190
175 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
176 195 200 205
178 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
179 210 215 220
181 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
182 225 230 235 240
184 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
185 245 250 255
187 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
188 260 265 270
190 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
191 275 280 285
193 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
194 290 295 300
196 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr
197 305 310 315 320
199 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
200 325 330 335
202 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
203 340 345 350

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205 Val

209 &lt;210&gt; SEQ ID NO: 4

210 &lt;211&gt; LENGTH: 1122

211 &lt;212&gt; TYPE: DNA

212 &lt;213&gt; ORGANISM: Homo sapiens

214 &lt;400&gt; SEQUENCE: 4

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215 atgggagcgt tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60
216 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcac 120
217 gtcacacctc gttgcgccat gcaggagacg acctcccgcc aggtggcctc ggccttcac 180
218 gtcacacctc gttgcgccat tgtgtgggaa aacctctctg tgctcattgc ggtggcccga 240
219 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggcgcc ctccgatcta 300
220 ctggcaggcg tggccttcgt agccaatadd ttgctctctg gctctgtcac gctgaggctg 360
221 acgcctgtgc agtgggttgc ccgggagggc tctgcctcca tcacgctctc ggcctctgtc 420
222 ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat 480
223 ggcagcgaca agagctgcgc catgctcttg ctcatcgggg cctcgtggct catctogctg 540
224 gtctcgggtg gcctgcccat ccttggctgg aactgcctgg gccacctcga ggcctgtctc 600
225 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtagccat cttctccatc 660
226 atcctgttgg ccactcgtgc cctgtacgtg cgcactactc gcgtggctcg ctcaagccac 720
227 gctgacatgg ccgcccgcga gacgctagcc ctgctcaaga cggtcacccat cgtgctaggc 780
228 gtctttatcg tctgttggct gccgccttc agcatcctcc ttctggacta tgctgtccc 840
229 gtccactcct gcccgatcct ctacaaagcc cactactttt tcgccgtctc caccctgaat 900
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232 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1080
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235 &lt;210&gt; SEQ ID NO: 5

236 &lt;211&gt; LENGTH: 375

237 &lt;212&gt; TYPE: DNA

238 &lt;213&gt; ORGANISM: Homo sapiens

240 &lt;400&gt; SEQUENCE: 5

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241 gggccatggc tcgagccgcc ccgacccccc gcgagcccgcc cttgtctgcg gcgtgactgg 60
242 agggccagat ggtcatcatg ggccagtgtc actacaacga gaccatcgcc ttcttctata 120
243 acaacagtgg caaagagctc agctccactc ggcggcccaa ggatgtggtc gtgggtggcac 180
244 tggggctgac cgtcagcgtg ctggtgctgc tgaccaatct gctggtcata gcagccatcg 240
245 cctccaaccg ccgcttccac cagcccactc actacctgct cggcaatctg gccgcggctg 300
246 acctcttcgc gggcgtggct acctcttctc catgttccac actgggtccc gcacagcccg 360
247 actttcactt gaggg 375

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249 &lt;210&gt; SEQ ID NO: 6

250 &lt;211&gt; LENGTH: 8

251 &lt;212&gt; TYPE: PRT

252 &lt;213&gt; ORGANISM: combination of rat and human.

254 &lt;400&gt; SEQUENCE: 6

255 Leu Leu Ala Ile Ala Ile Glu Arg

256 1 5

259 &lt;210&gt; SEQ ID NO: 7

260 &lt;211&gt; LENGTH: 22

261 &lt;212&gt; TYPE: DNA

262 &lt;213&gt; ORGANISM: combination of rat and human.

264 &lt;220&gt; FEATURE:

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265 <221> NAME/KEY: misc_feature
266 <222> LOCATION: (6) /
267 <223> OTHER INFORMATION: The n at position 6 can be g or c.
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (12) /
272 <223> OTHER INFORMATION: The n at position 12 can be c or t.
274 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
276 <222> LOCATION: (17) /
277 <223> OTHER INFORMATION: The n at position 17 can be c or t.
279 <220> FEATURE:
280 <221> NAME/KEY: misc_feature
281 <222> LOCATION: (21) /
282 <223> OTHER INFORMATION: The n at position 21 can be a or c.
284 <400> SEQUENCE: 7
W--> 285 ctccctngcca tngcatngag ng 22
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 8
289 <212> TYPE: PRT
290 <213> ORGANISM: combination of rat and human.
292 <400> SEQUENCE: 8
293 Leu Leu Leu Leu Asp Ser Thr Cys
294 1 5
297 <210> SEQ ID NO: 9
298 <211> LENGTH: 22
299 <212> TYPE: DNA
300 <213> ORGANISM: combination of rat and human.
302 <220> FEATURE:
303 <221> NAME/KEY: misc_feature
304 <222> LOCATION: (4) /
305 <223> OTHER INFORMATION: The n at position 4 can be c or g.
307 <220> FEATURE:
308 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (6) /
310 <223> OTHER INFORMATION: The n at position 6 can be a or c.
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (7) /
315 <223> OTHER INFORMATION: The n at position 7 can be a or g.
317 <220> FEATURE:
318 <221> NAME/KEY: misc_feature
319 <222> LOCATION: (8) /
320 <223> OTHER INFORMATION: The n at position 8 can be a or c.
322 <220> FEATURE:
323 <221> NAME/KEY: misc_feature
324 <222> LOCATION: (9) /
325 <223> OTHER INFORMATION: The n at position 9 can be a or g.
327 <220> FEATURE:

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\05012001\I274752D.raw

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9